IN THE CLAIMS

Claim 1 (original): A method for selectively binding micromolecules having a lysine functionality comprising the steps of:

providing a sample containing one or more species of macromolecules, each having a lysine functionality;

providing a binding reagent having the formula

X-NH-C(=NH)-OR

or

X-L-NH-C(=NH)-OR

where X is an affinity label that selectively binds to a capture reagent, R is a residue group, and L is a linker moiety;

introducing the binding reagent to the sample so as to effect a guanidination reaction between the binding reagent and said one or more species of macromolecules, thereby producing one or more affinity label containing homoarginine derivatives;

optionally modifying the affinity label containing homoarginine derivatives to produce further affinity label containing homoarginine derivatives; and

capturing affinity label containing homoarginine derivatives using the capture reagent that selectively binds X.

Claim 2 (original): A method for analysing one or more proteins, protein functions and/or peptides in one or more samples comprising the steps of:

providing a binding reagent having the formula

X-NH-C(=NH)-OR

or

X-L-NH-C(=NH)-OR

where X is an affinity label that selectively binds to a capture reagent, R is a residue group, and L is a linker moiety;

introducing the binding reagent to the one or more samples so

as to effect a guanidination reaction between the binding reagent and proteins and/or peptides having a lysine functionality, thereby producing one or more affinity label containing homoarginine derivatives;

optionally modifying the affinity label containing homoarginine derivatives to produce further affinity label containing homoarginine derivatives;

capturing affinity label containing homoarginine derivatives using the capture reagent that selectively binds X; and

performing an analysis of affinity label containing homoarginine derivatives.

Claim 3 (original): A method according to claim 2, in which the step of modifying the homoarginine derivatives comprises converting proteins present into peptides.

Claim 4 (currently amended): A method according to claim 2 ~~or claim 3~~, in which the proteins, protein functions and/or peptides are identified by the analysis of the affinity label containing homoarginine derivatives.

Claim 5 (original): A method according to claim 4, in which the analysis comprises the step of comparing data generated by an analytical technique with sequence databases.

Claim 6 (original): A method according to claim 2, in which relative expression levels of proteins in two or more samples containing proteins are determined comprising the steps of:

providing a series of binding reagents having the formula

X-NH-C(=NH)-OR

or

X-L-NH-C(=NH)-OR

where X is an affinity label that selectively binds to a capture reagent, R is a residue group, and L is a linker moiety, and wherein the chemical formulae of the binding reagents in the series are identical but each binding

reagent in the series comprises a different combination of isotopes so that binding reagents in the series are isotopically labelled by way of the molecular mass of each binding reagent in the series being different to the molecular masses of the other binding reagents in the series;

introducing a different binding reagent from the series to each sample so as to effect, in each sample, a guardination reaction between a binding reagent and moieties having a lysine functionality, thereby producing a plurality of isotopically labelled, affinity label containing homoarginine derivatives;

combining the samples;

optionally converting proteins into peptides;

capturing affinity label containing homoarginine derivatives using the capture reagent that selectively binds X; and

performing an analysis of affinity label containing homoarginine derivatives in which the relative abundances of a subset of homoarginine derivatives which differ only by virtue of their isotopic labelling are measured, thereby determining the relative expression levels of the protein from which the subset of homoarginine derivatives originated.

Claim 7 (original): A method according to claim 6 in which the step of converting proteins into peptides comprises converting proteins present in the affinity label containing homoarginine derivatives into peptides.

Claim 8 (currently amended): A method according to claim 6 ~~or claim 7~~, in which proteins, protein function and/or peptides are identified by the analysis of the affinity label containing homoarginine derivatives.

Claim 9 (original): A method according to claim 8, in which the analysis comprises the step of comparing data generated by an analytical technique with sequence data.

Claim 10 (currently amended): A method according to claim 2 ~~any one of claims 2 to 9~~, in which the analysis comprises mass spectrometric analysis.

Claim 11 (original): A method according to claim 10, in which the mass spectrometric analysis comprises tandem mass spectrometry.

Claim 12 (currently amended): A method according to claim 2 ~~any one of claims 2 to 11~~, further comprising the step of releasing captured affinity label containing homoarginine derivatives from the capture reagent prior to the step of performing an analysis.

Claim 13 (original): A method according to claim 12 in which the capture reagent comprises part of a chromatographic separation system which separates chemically different affinity label containing homoarginine derivatives.

Claim 14 (original): A method according to claim 13 in which the chromatographic separation system utilises liquid chromatography.

Claim 15 (original): A method according to claim 13 in which the chromatographic separation system utilises gas chromatography.

Claim 16 (original): A method according to claim 2 in which absolute quantification of the proteins and/or peptides is obtained.

Claim 17 (currently amended): A method according to claim 1 ~~any previous claim~~ in which R is an alkyl group.

Claim 18 (original): A method according to claim 17 in which R is CH_3.

Claim 19 (currently amended): A method according to claim 1 ~~any previous claim~~ in which X is an alkyl group.

Claim 20 (original): A method according to claim 19 in which X is CH_3.

Claim 21 (original): A method according to claim 20 in which the binding agent is $CH_3CONHC(=NH)OCH_3$.

Claim 22 (original): A reagent for selectively binding molecules having a lysine functionality having the formula

X-NH-C(=NH)-OR

or

X-L-NH-C(=NH)-OR

where X is an affinity label that selectively binds to a capture reagent, R is a residue group, and L is a linker moiety.

Claim 23 (original): A reagent according to claim 22, in which X is biotin or a modified biotin.

Claim 24 (original): A reagent according to claim 23 in which X is an alkyl group.

Claim 25 (original): A reagent according to claim 24 in which X is CH_3.

Claim 26 (currently amended): A reagent according to claim 22 ~~any of claims 22 to 25~~, in which R is an alkyl group.

Claim 27 (original): A reagent according to claim 26 in which R is CH_3.